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Pred. No. is the number of results predicted by chance to have a

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SUMMARIES

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AX139125 Sequence 1 from Patent EP1085093. AX139125 AX139125. AX139125.1 GI:14274801 human. human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 164) Blumenberg, M. and Gazel, A. M. Genes and polynucleotides associated with ultraviolet radiation-mediated skin damage and uses thereof	

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                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2157)
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/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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Mammalia; Eutheria; Primates;
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HSA311797
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   1161 CAAAATGAGCACAGCAGCACCTATGCCTGGATGGCCCCCGAAG
                                                                            1101
                                                                                                                                                  1041 GCACCGGGACCTCAAGTCCAGCAACATTTTGCTACTTGAAGAGATAGAACATGATGATGACAT 1100
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                                       121
                                                                                                                                                                                                                            Local Sin hes 155;
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                                                                                                                                                                                       1 GCACCGGGACATCAAGGCAGGAAATATTTTGCTACTTGAGAAGATAGAACATGATGACAT 60
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                                                                          CTGCAATAAAACTTTGAAGATTACAGATTTTGGGTTGGCGAGGGAATGGCACAGGACCAC 1160
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                                     CAAAATGAGCACAGCAGCACCTATGCCTGGATGGCCCCAGAAG
                                                                                           CTGCAATAAAACTTTGAAGATTACAGATTTTGGGTTGGCGAGGGAATGGCACAGGACCAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens mRNA for mixed lineage kinase 4alpha (MLK4ALPHA gene).
AJ311797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (12-APR-2001) Kashuba V., Mi
Center, Karolinska Institute, Box 280,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kvasha,S., Protopopov,A., Rynditch,A., Zabarovsky,E. and Kashuba,V. \mathtt{MLK4}, a new member of mixed lineage kinases
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                              WELLTGEVPYRGIDGLAVAYGVAVNKLTLPIPSTCPEPFAKLMKECWQQDPHIRPSFA
LILEQLTAIEGAVMTEMPQESFHSMQDDWKLEIQQMFDELRTKEKELRSREEELTRAA
LQQKSQEELLKRREQQLAEREIDVLERELNILIFQLNQEKPKVKKRKGKFKRSRLKLK
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/evidence=experimental
/product="mixed lineage kinase 4alpha"
/protein_id="CAC84639.1"
/protein_id="CAC84639.1"
/db_xxef="GI:17736729"
/db_xxef="GI:17736729"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="MLK4ALPHA"
262. .1974
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262. .1974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AASPAPPPSRPSSPYHVAFERLELKELIGAGGFGQVYRATWQGQEVAVKAARQDPEQD
AAAAAESVRREARLFAMLRHPNIIELRGVCLQQPHLCLVLEFARGGALNRALAAANAA
PDPRAPGPRRARRIPPHYLVNWAVQIARGMLYLHEEAFVPILHRDLKSSNILLLEEIE
                                                                                                                                                                                                                                                                                                                                                                            DGHRISLPSDFQHKITVQASPNLDKRRSLNSSSSSPPSSPTMMPRLRAIQCELSALPP
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/db_xref="taxon:9606"
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 121 CAAAATGAGCACAGCAGGCACCTATGCCTGGATGGCCCCAGAAG 164
                                                                          61 CTGCAATAAAACTTTGAAGATTACAGATTTTGGGTTGGCGAGGGAATGGCACAGGACCAC 120
                                                                                                                                                  1 GCACCGGGACATCAAGGCAGGAAATATTTTGCTACTTGAGAAGATAGAACATGATGACAT 60
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91.2%; 94.5%;

Score 149.6; Pred. No. le Mismatches

1e-33;

DB 9 9;

Length 4667; Indels

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Homo sapiens mRNA for mixed lineage kinase 4beta (MLK4BETA gene).
AJ311798
AJ311798.1 GI:17736730
mixed lineage kinase 4beta; MLK4BETA gene.
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MLK4, a new member of mixed lineage kinases
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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AAAAAESVRREARLFAMLRHPNIIELRGVCLQQPHLCLVLEFARGGALMRALAAANA
PDPRAPGRRSRS PHYVLVMRAVQIARGHGVYRATWQGGALMRALAAANA
PDPRAPGRRARRIPHVLVMRAVQIARGHLVLHEBARVPILHRDLKSSNILLLEEIE
HDDLCNKTLKITDGELAREMHRTTKMGTSGTGTVAMMAPBVIKSSLFSKGSDIMSGGVLL
WELLIGEVPYRGIDGLAVAYGVAVNKLTLPIPSTCPEPEAKLMKECWQQDPHIRPSFA
LILEQLTALEGAVWTEMPQESSHSMQDDWKLEJQNDVDELATKEKELRSREEELTRAA
LQQKSQEELLKRREQQLAEREIDVLERELNILIFQLNQEKPKVKKRKGKFKRSRLLKLK
DGHRISLFSDEPHKTTVQASPRLDKRRSLNSSSSSPESSTMWERLRAIQLTSDESNK
TWGRNTVFRQEEFEDVKRNFKKKGCTWGPNSIQMKDRTDCKERIRPLSDGNSPWSTIL
IKNQKTMPLASIFYDQPGSCEEPKKLSPDGLHERBKQLJEGSAFDFALEDLR
PAERAGSWEEAASANAATVTIEMAPTNSLSRSPORKTESALYCGTVLASVALGLDLR
ELHKAQAAEEPLPKEEKKREGIFQRASKSRRSASPFTSLSSTCGEASSPPSLPLSSA
LGILSTPSESTKCLLQMSSEDPLVDSAFVTCDSEMLTPDFCFTAFGSGREPALMERLD
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ALYDYEARGEDELSLRRGQLVEVLSQDAAVSGDEGWWAGQVQRRLGIFPANYVAPCRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="MLK4BETA"
262. .3372
                                                                              CVVGRPGPHPTQFLAAKERTKSHVPSLLDVDVEGQSRDYTVPLGRMRSKTSRPSIYEL
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LPLCPSPAPHSHLPREVSPKKHSTVHIVPQRRPASLRSRSDLPQAYPQTAVSQLAQTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=experimental
/product="mixed lineage
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Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/HGP/Chr1
RP5-862P8 is from the library RPCI-5 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For furth details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (31-MAY-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL133380 118632 bp DNA linear PRI 29-NOV-2000 Human DNA sequence from clone RP5-862P8 on chromosome 1q42.2-43 Contains a 40S ribosomal protein S7 pseudogene, start of a gene for a novel protein (similar to C.elegans and D.melanogaster), a gene similar to MAP3K10 (mitogen-activated protein kinase kinase kinase li), STSs, GSSs and a CpG island, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          During sequence assembly data is compared from overlapping clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG; CpG island; protein kinase; Ribosomal Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL133380.5 GI:8217443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence is the entire insert of clone RP5-862P8 Location/Qualifiers
/note="190 copies 2 mer tt 74% conserved"
complement(1810. .2413)
/note="match: STS: Em:D11774"
complement(1812. .1928)
                                                                                                                                                                                                                                                                                                     /clone_lib="RPCI-5" 323. .682
                                                                                                                                                     complement(1793.
                                                                                                                                                                                                    complement(1784.
                                                                                                                                                     /note="match: GSS: Em:AQ887379"
complement(1793. .1994)
                                                                                                                                                                                                    /note="MIR repeat: matches 45.
complement(1784. .2072)
                                                                                                                                                                                                                                                                                                                                                                      /chromosome="1"
/map="q42.2-43"
                                                                                                                            /note="match: GSS: Em:AQ384546"
                                                                                                                                                                                                                                                                          /note="THE1B repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                    /clone="RP5-862P8"
                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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                                                                                                             1850
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Primates;
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                                                                                                                                                                                                                             262
                                                                                                                                                                                                                                                                          .362 of consensus"
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                                                                                                                                                                                                                                                                /evidence=not_experimental
/product="dd86281.2 (5' end of gene encoding novel protein
similar to C.elegans and D.melanogaster)"
/protein_id="CAC17570.1"
/db_xref="GI:11493212"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5181. .5494
/note="AluSx repeat: matches 1.
complement(6410. .6697)
                                                    /note="L2 repeat: matches 2157.
11593. .11897
                                                                                                                  /PLANIM

JB440. 9031

J840. 9031

/note="96 copies 2 mer ct

10240. 10362

10240. 10362
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="dJ862P8.2 (5' end of gene encoding novel protein similar to C.elegans and D.melanogaster)"
/evidence=not_experimental
complement(<8312. .8464)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MIR repeat: matches 1. .247 of consensus" 6974. .7178
/note="MIR repeat: matches 34. .256 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 2. .142 of consensus"
4207. .4313
                                                                                                   10558.
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/gene="dJ862P8.2
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/note="match: GSS: Em:AQ177047"
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/gene="dJ862P8.1"
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match: protei
    /note="AluSx repeat: matches 1.
11942. .12373
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/gene="dJ862P8.1"
                                                                                                                                                                                                                                            translation="MVSQVLQLLRQGVWAALTGGWYHDPEQSKFTNSCHLYLWLFLLL/
                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="dJ862P8.2"
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complement(6422. .6787)
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/note="match: GSS:
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1875. .2308
                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                  'note="match: proteins: Tr:046074"
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match: cDNAs: Em:X74803 Em:U16258 Em:V01442 Em:M77233
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proteins: Sw:P02362 Sw:P23821 Sw:P50894"
                                                                                                   .10791
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                             .312 of consensus"
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                                                                                           TITTGCTACTTGAGAAGATAGAACATGATGACATCTGCAATAAAACTTTGAAGATTACAG 59487
                                                                                                              TTTTGCTACTTGAGAAGATAGAACATGATGACATCTGCAATAAAACTTTGAAGATTACAG 86
                                 ATTTTGGGTTGGCGAGGGAATGGCACAGGACCACAAATGAGCACAGCAGGAGCACCTATG 146
                ATTTTGGGTTGGCGAGGGAATGGCACAGGACCACCAAAATGAGCACAGCAGGCACCTATG
                                                                                                                                                                                         Similarity
                                                                                                                                                                      Conservative
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14285...14806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L1M4 repeat: matches 2693.
16241. .16506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14684
                                                                                                                                                                                                                                                                                                                                                                    /note="AluSx repeat: matches 1. 23101. .23421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="AluJb repeat: matches 24. .288 of consensus"
16509. .16548
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                                                                                                                                                                                                                                                                                             23643.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18741.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="20 copies 2 mer at 77% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="HAL1 repeat: matches 935. .1051 of consensus"
                                                                                                                                                                                                                                                                                                                                   23468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MSTB repeat: matches 1.
20631. .20842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19580. .19641
/note="L1MB8 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="L1PA4 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note-"L1M4 repeat: matches 2375.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="51 copies 2 mer aa 60% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="AluSx repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="L1MEc repeat:
                                                                                                                                                                                                                                                                        'note="MSTB
                                                                                                                                                                                                                                                                                                                                                    note="I1M4 repeat: matches 2740.
                                                                                                                                                                                                                                                                                                                                                                                                                               'note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e-"AluSx repeat:
                                                                                                                                                                                       83.2%;
99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .16185
                                                                                                                                                                                                                                               MSTB repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .16726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIR repeat: matches 22.
.21474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .21873
                                                                                                                                                                                                                                                                                         LLT1J repeat: matches 104. .191 of consensus" 24023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat:
                                                                                                                                                                    Score 136.4; | Pred. No. 1.1e 0; Mismatches
                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Em: AQ476745"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       matches 842. .935 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          matches 6113. .6174 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        matches 1. .309 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    matches 6057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  matches 2311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   matches 5980.
                                                                                                                                                                                         1.1e-29;
                                                                                                                                                                                                              DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .245 of consensus"
                                                                                                                                                                                                                                                                        .418 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .312
                                                                                                                                                                                                                                                                                                                                                                                           .311 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   .289 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2375 of consensus"
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                                                                                                                                                                                                          Length 118632;
                                                                                                                                                                                                                                                                                                                                                    .3046 of consensus
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                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MCC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 35 Row: d Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (18-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (
DNA Sequencing by: Baylor College of Medicine Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BC021891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus, Similar to mitogen-activated protein kinase ki kinase 9, clone MGC:27778 IMAGE:3156324, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, '
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                 VHVDFERLELKËLIGAGGFGQVYRATWQGQEYAVKAARRDPRODAADAAAESVERREARL
FAMLRHPNI IQLRGVCLRQPHLCLVLEFARGGALNRALAAASDPAAFGPRARRIPP
QVLVWHAVQI ARGMIX HLEEAVVP LILHRDLKSKSNILLLEKI EHDDICNKTLKITDFGL
AREWHRTTRMSAAGTY AWMAPEVIRSSLFSKGSDINSYGVLMELLTGEVPYRGIDGL
AVAYGYAVKLTLPI BSTCPEFSKLMKECWEDDPHIR PSFALLIQQLTA I EEAVLTIN
MPQESSFHSMGDÜWKLELJOMFSBLFTKENELRSREELSRAALQOKSQELLLRREQQL
ABREEIDVLERELNVLIFQLSQEAPHVKKRKGBFRRGBLRLXDGHRISLPSDEJKKITV
AEREIDVLERELNVLIFQLSQEAPHVKKRKGBFRRGBLRLXDGHRISLPSDEJKKITV
                                                                                                                                                                      /product="similar to mitogen-activated protein kinase kinase 9"
kinase kinase 9"
/protein_id="AAHZ1891.1"
/db_xref="GI:18257338"
/translation="MALPVAEGTADTPLSPARDDSGSTSSGMWAALYDYEARGEDELS
/translation="MALPVAEGTADTPLSPARDDSGSTSSGMWAALYDYEARGEDELS
LRRGQIVEVLSQDAAVSGDEGWWAAGQVQRRLGIFPASYVAPGGPVPPPAPPPRRPCSP
                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Mammary tumor. C3(1)-Ta ductal carcinoma. 5 month old virgin
                    QASPTLDKRRSSDSGLCSPPGSPLMLPRLRAIQLTSDENNKTRGRNMVFRQEDFEDVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
{	t RSFKKKGCTWGPSSVQTKERPEGRERVRPLSDGNSPWSSLLIKSQKTTPLASLFVDQF}
                                                                                                                                                                                                                                                                                                                                     /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /map="EVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                             /codon_start=]
                                                                                                                                                                                                                                                                                                                                                      /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="NCI_CGAP_Mam6"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="MGC:27778 IMAGE:3156324"
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                                                                                                                                                                                                                                                                                                                                     pCMV-SPORT6"
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R.G., Muzny, D.M
                                                                                                                                                                                                                                                                                                                                                                                               mouse."
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                                                                                                                                                                                                                                                                                                                                                                                                                    Infiltrating
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                                                                                                                                                                                                                         RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Camarata, J., Campopiano, Chang, J., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, P., Coke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ginde, S., Gord, S., Goyette, M., Graham, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazzares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., McCernthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norba, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, T., Zambek, L., Zimmer, A., and Zadv, M., Young, G., Zainoun, T., Zambek, L., Zimmer, A., and Zadv, M.
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                      Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B.,
                                                                                                            Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 168795)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC102420 168795 bp
Mus musculus clone RP24-553021,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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                                                                                      (bases 1 to 168795)
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ASRCQSSPSSLLRQPSAGRAPSGGSTLLLPSAPSHSSKSSLSMKCLLQAGKEESSLGN
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                                                                                                                                                                                                                   Zembek, L.,
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Pred. No. 3.5e-25;
                                                                                                                                                                                                                Zimmer, A. and Zody, M.
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Boguslavkiy,L.,
B., Choepel,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WORKING DRAFT SEQUENCE,
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25
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Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Kalls, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P.,
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
Yenhek, I., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, Ma 02141, USA On Aug 21, 2002 this sequence version replaced gi:17061506. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html Genome Center
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Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Due; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 161900 bases at least Q40
Consensus quality: 165140 bases at least Q30
Consensus quality: 165006 bases at least Q20
Insert size: 176000; agarose-fp
Insert size: 166395; sum-of-contigs
Quality coverage: 5.7 in Q20 bases; sum-of-contigs
Quality coverage: 6.1 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as soon as it is available and the accession number will be preserved.
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Contact: sequence_submissions@genome.wi.mit.edu
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11713
11813
                                                                                                                                                               14078
                                                                                                                                                                                                                                       7216 8963: contig of 1748 bp
8964 9063: gap of 100 bp
9064 11712: contig of 2649 bp
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995 2169: co
                                                                                                                                                                                                                                                                              5627: contig of 1020 bp in 1e
5627: gap of 100 bp
728 7115: contig of 1388 bp in len
16 7215: gap of 100 bp
16 8963: contig of 1388 bp in len
16 8963: contig
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17221: contig of 3044 bp
17321: gap of 100 bp
19510: contig of 2189 bp
19610: gap of 100 bp
23807: contig of 4197 bp
                                                                                                                                                                                                                                                                                                                                                                                              100 bp
4507: contig of 1339 bp
4607: gap of 100 bn
5627: conti-
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4507: contig of 799 bp in length
                                                                                                                                             11812: gap of 100 bp
14077: contig of 2265 b
14177: gap of 100 bp
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contig of 1175 bp in length
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FEATURES
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137005 137104:
137105 168795
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80212 9496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment"
9064. .11712
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment"
31509. .35352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment"
17322. 19510
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/db_xref="taxon:10090"
/clone="RP24-553021"
                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_fragment"
35453. .40317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_fragment"
23908. .26130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="assembly_fragment"
19611. .23807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_fragment"
11813. .14077
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/note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40417: gap
47500:
/note="assembly_fragment"
67293. .80111
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137004: contig of 20795 bp in length
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116109: contig of 21042 bp in
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SOURCE
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
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Local Similarity 85.58;
Carron, T.E., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Carron, T.E., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., David, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., David, M.L., Davis, C., Davy-Carroll, L., Dederich, M.J., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, K.J., Durbin, K.J., Durbin, K.J., Delaney, K.R., Delgado, D., Edwards, C.C., Elhaj, C., Escotto, M., Earlhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earlhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earlhart, C., Edgar, D., Edwards, C., Charles, N., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gabisi, A., Gao, J., Foster, P., Frantz, P., Falls, T., Ferraguto, D., Edwards, M., Holloway, C., Hollins, B., Hernandez, O., Hodges, M., Holloway, C., Hollins, B., Hernandez, S., Huber, J., Hulyk, S., Hamilton, K., Hernandez, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Kartovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, X., Lucier, A., Lucier, R., Lund, R., Ma, J., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Lund, R., Ma, J., Land, R., Ma, J., Massey, E., Mahhney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Massey, E., Mahhney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Massey, E., Mahhney, E., McLeod, M.P., Meador, M., Okwuonu, G., Oragunye, N., Oriedo, R., Pace, A., Payton, B., Perey, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Peters, L., Pet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTGGATGGCTCCCGAGG 21521
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Rattus norvegicus clone CH230-234D24, *** SEQUENCING
***, 49 unordered pieces.
AC112003
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AC112003.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
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On Jul 12, 2002 this sequence version replaced gi:18701953
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3 (bases 1 to 96101)
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NOTE: This is a 'working draft' sequence. It currently consists of 49 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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be preserved.
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 49084 bases at least Q40
Consensus quality: 53702 bases at least Q30
Consensus quality: 57526 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (03-APR-2000) Molecular and Genetic Medicine, University of Sheffield, Royal Hallamshire Hospital, Glossop Road, Sheffield S10 2JF, United Kingdom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens mixed lineage kinase MLK1 mRNA, AF251442
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McNee, J.J. and Guesdon, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA sequence and gene Unpublished 2 (hases 1 to 3931)
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/db_xref="taxon:10116"
/clone="CH230-234D24"
/ 21808 c 22462 g 23062 t
LLAASWVVP ID I EEDEDSEGPGSGESKLQHSPSQSYLCI PFPRGEDGDGPSSDGIHEE
PTVNUSATSTPQLTPTWSLKRGGAHHRRCEVALLGCGAVLAATGEDLLEAGKCQLL
PLEEPEPPAREEKKREGLFORSSRPRRSTSPPSRKLFKKEEPMLLLGDPSASLTLLS
LSSISECNSTRSLLRSDGEI VVY EMPVSPVEAPPLSPCTHNPLVNVRVERFKEDPNQ
SLTPTHVTLTTPSQPSSHRRTPSDGALKPETLLASRSPSSNGLSPSPGAGMLKTPSPS
                                                                                             NPDPHSRPSFTNILDQLTTIEESGFFEMPKDSFHCLQDNWKHEIQEMFDQLRAKEKEL
RTWEEELTRAALQQKNQEELLARREQELAERELDILERELNIIHQLCQEKPRVKRK
GKFRKSRLKLKDGNRISLPSDFQHKFTVQASPTDMDKRKSLINGRSSPASPTIIFRK
AIQLTPGESSKTWGRSSVVPKEEGEEEEKRAPKKGRTWGPGTLGQKELASGDEGSPQ
RREKANGLSTPSESPHFHLGLKSLVDGYKQWSSSAPNLVKGPRSSPALPGFTSLMEMA
                                                                                                                                                                                          GOLNQRVGIFPSNYVTPRSAFSSRCQPGGEDPSCYPPIQLLEIDFAELTLEEIIGIGG
FGKVYKAFWIGDEVAVKAARHDPDEDISQTIENVRQEAKLFANLKHENIIALRGYCLK
EPNLCLVMEFARGGELNRVLSGKRIPPDILVMAVQIARGMNYLHDEAVFUIHDELK
SSNILLIQKVERGDLSNKILKITDFGLAREWHRTTKMSAAGTYXWMAPEVIRASMESK
SSNILLIQKVERGDLSNKILKIDFGLAREWHRTTKMSAAGTYXWMAPEVIRASMESK
GSDVWSYGVLLWELLTGEVPFRGIDGLAVAYGVAMNKLALPIPSTCPEPFAKLMEDCW
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Location/Qualifiers
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<1. .3202
                                                                                                                                                                                                                                                                                         /product="mixed lineage kinase MLK1"
/protein_id="AA644591.1"
/db_xref="GI:12005724"
/translation="plpyWTAVFEYEAAGEDELTLRLGDVVEVLSKDSQVSGDEGWWT
                                                                                                                                                                                                                                                                                                                                                                       /codon_start=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                        /note="protein kinase"
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U07747
                                                                                                                                                                                                                                                                                                                                                                                                Submitted (15-MAR-1994) Paul
Point San Bruno Blvd., South
Location/Qualifiers
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domain-containing proline-rich kinase with serine/threonine kinase
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to
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SPSHARSTSPANSSSTETPSNLDSCFASSSSTVEERPGLPALLPFQAGPLPPTERTLL
DLDAEGGSQDSTVPLCRAELNTHRPAYVETQQEFWS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chem.
VWTALFDYEDSGODELALRKGDRVEVLSRDAAISGDEGWWAGOVGGOVGIFPSNYVSR
GGGPPPCEVASFOELRLEEVIGIGGFGKVYRGSWRGELVAVKAARODPDEDISVTAES
VRQEARLFAMLAHPNIIALKAVCLEEPNLCLVMEYAAGGPLSRALAGRRVPPHVLVNW
                                                                                                                                   /note="submitter comments: serine/threonine
kinase, proline-rich, src-homology 3 (SH3) (
leucine/isoleucine zipper motifs"
                                                                                                                                                                                        /standard_name="src-homology 3 (SH3) domain-containing
proline-rich kinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:464027
                                                                 /product="serine/threonine protein kinase"
/protein_id="AAAA19647.1"
/db_xref="GI:464028"
                                                                                                                                                                                                                                                                                                             /cell_line="CMK11-5"
/clone_lib="gt 10"
                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                       /codon_start=1
                                                                                                                                                                                                                            /standard_name="SPRK"
                                                                                                                                                                                                                                         /gene="sprk"
                                                    translation="MEPLKSLFLKSPLGSWNGSGSGGGGGGGGGGRPEGSPKAAGYANP/
                                                                                                                                                                                                                                                                         gene="sprk"
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73.6%;
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No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                    J. Godowski, Genentech, Inc.,
San Francisco, CA 94080, USA
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.7e-17;
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domain,
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ORGANISM
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AX399680
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ORIGIN
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Best Local Sim
Matches 113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAATGAGCACAGCAGGCACCTATGCCTGGATGGCCCCAGAAG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCAATAAAACTTTGAAGATTACAGATTTTGGGTTGGCGAGGGAATGGCACAGGACCACC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACCGTGATCTCAAGTCCAACAACATTTTGCTGCTGCAGCCCATTGAGAGTGACGACATG 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cancer associated protein kinases and their uses Patent: WO 0224947-A 1 28-MAR-2002; KINETEK PHARMACEUTICALS INC (CA); UNIV BRITISH CO
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3558 bp
Sequence 1 from Patent WO0224947,
AX399680
                                                                                                                                                                                                                                                                                                                                                                                               Delaney,A.D. and Yoganathan,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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AVQIARGMHYLHCEALVPVIHRDLKSNNILLLQPIESDDMEHKTLKITDFGLAREWH
                VWTALFDYEPSGQDELALRKGDRVEVLSRDAAISGDEGWWAGQVGGQVGIFPSNYVSR
GGGPPPCEVASFQELRLEEVIGIGGFGKVYRGSWRGELVAVKAARQDPDEDISVTAES
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                                                                                                                                                                                                             /db_xref="taxon:9606"
482. .3025
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HSWQEGWKRE I QGLFDELFAKERELLSREELITRAKER GRQADAGULRREHLLAQWEL
EVFERELTILLQQUDRERPHVERRETT FKRSKLRARDGEER SWPLDFKHR TYVQAS
ELDRERRAVEFYGPGDSPTFPRERAIQLEPAEPGQAWGRQSPRRLEDSSNGERRACWAW
GLDRRRRNVEFYGPGDSPTFPRERAIQLEPAEPGQAWGRQSPRRLEDSSNGERRACWAW
GPSSPKPGEAQNGRRRSRMDEATWYLDSDDSSPLGPSTFP PAPELEPEEPK
RPVPAERGSSGTFKLIQRALLAGTALLASTGLIGRDLOPGGGFGERGESPTFPFFFE
RPVPAERGSSGTFKLIGTSLKTFDSPFTPAPLLLDLGIFVGQRSAKSPRREEEPRGGTVS
                                                                                                                                                                                  /note="unnamed protein product"
                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="kinase domain"
1710. .1896
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RRAPWTLFPDSDPFWDSPPANPFQGGPQDCRAQTKDMGAQAPWVPEAGP"
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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/note="32 A residues"
1207 c 1143 g
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/gene-"sprk"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Leucine/Isoleucine zipper region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="sprk"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="sprk"
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Pred. No. 5.6e
0; Mismatches
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MEDLINE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 CACCGGGACATCAAGGCAGGAAATATTTTTGCTACTTGAGAAGATAGAACATGATGACATC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAATGAGCACAGCAGGCACCTATGCCTGGATGGCCCCAGAAG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGCACAAGACCCTGAAGATCACCGACTTTGGCCCTGGCCCGAGAGTGGCACAAAACCACA 1315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MLK-3: identification of a widely-expressed protein kinase an SH3 domain and a leucine zipper-basic region domain oncogene 9 (6), 1745-1750 (1994)
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (tissue library: lambda gt10) thymus cDNA to mRNA.
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                                                                                                                                                                . . 1932;
/translation="MEPLKSLFLKSPLGSWNGSGSGGGGGGGGGRPEGSPKAAGYANP
VWTALFDYEPSGODELALRKGDRVEYLSRDAALSGDEGWWAGGYGGYVGIFPSMYVSR
GGGPPPCEVASFQELRLEEDYIGIGGFGKVYRGSWRGELVAVKAARQDEDEDISVTAES
VRQEARLFAMLAHPNIIALKAVCLEEPNLCLVMEYAAGGPLSRALAGRRVPPHVLVNW
                                                                                                                                                                                                  /standard_name="PTK-1, sprk"
/note="amino acid feature: SH3 domain, bp 613 . . 78
amino acid feature: leucine zipper basic region, bp
                                                                                                                                                                                                                                                                                     /gene="MLK-3"
482. .3025
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AVNKITLPISTGPEPFAQLMADCWAQDPHRRPDFASIIQQLEALEAQVILEEMPRDSF
HSMQEGMKREIGGLEFDELRAKKELLSREEELIRAARBORSQAEQLRAREHLLAQWEL
EVFERELTLLOQVDRERPHVERRRGTFKRSKLRARDGGERISMPLDFKHRITVQASP
GLDRRRWTEVGPGDSPTFPRFAIQLEABEPGQAWGROSPRLEDESSMGERRACWAW
GPSSPKPGEAQMGRRASFANDEATWYLDSDDSSPLGSPETPALMGNPPRSLEPEEPA
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                                                                               /product="protein kinase"
/protein_id="AAA59859.1"
/db_xref="GI:488296"
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PPPGTSRSAPGTPGTPRSPPLGLISRPRPSPLRSRIDPWSFVSAGPRPSPLPSPQPAP
RRAPWTLFPDSDFFWDSPPANPFQGGPQDCRAQTKDMGAQAPWVPEAGP*
                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                      /gene="MLK-3"
                                                                                                                                                                                                                                                                                                                                                   /tissue_type="thymus"
/tissue_lib="lambda g1
                                                                                                                                                                                                                                                                                                                                                                                              /map="11 q13.1-13.3"
                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                    ′organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                    .3558
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                                                                                                                                                                                     amino
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(MLK-3) mRNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 83; DB of Pred. No. 5.6e 0; Mismatches
                                                                                                                                                                                     acid
                                                                                                                                                                                                                                                                                                                                                 gt10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                   feature: proline-rich region,
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complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRI 07-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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BC011263
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AUTHORS
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VERSION
                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
ORGANISM
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Best Local
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                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 AAAATGAGCACAGCAGGCACCTATGCCTGGATGGCCCCAGAAG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
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nes 113; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 CACCGGGACATCAAGGCAGGAAATATTTTGCTACTTGAGAAGATAGAACATGATGACATC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAATGAGTGCCGCGGGCACCTACGCCTGGATGGCTCCTGAGG 1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCAATAAAACTTTGAAGATTACAGATTTTGGGTTGGCGAGGGAATGGCACAGGACCACC 121
                                                                      Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNI at: http://image.llnl.gov Series: IRAK Plate: 12 Row: o Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 4505194.
                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., I
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck,
                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genom Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (25-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BC011263
BC011263.1 GI:15030036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                      Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                 Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: MGC help
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Institute, 31 Center Drive, Room 11AO3, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 3603)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1263 3603 bp mRNA linear PRI 30-JU sapiens, Similar to mitogen-activated protein kinase kin se_ll, clone MGC:17114 IMAGE:4215281, mRNA, complete cds.
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PPPGTSRSAPGTPGTPRSPPLGLISRPRPSPLRSRIDPWSFVSAGPRPSPLPSPQPAP
RRAPWTLFPDSDPTWDSPPANPFQGGPQDCRAQTKDMGAQAPWVPEAGP"
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AVNKLTLPIFSTCPEPFAQLMADCWAQDHRRPDFASIQQLEALEAQVILEMPRDSF
HSMQDGWKREIQGLFDELRAKEKELLSREEELITAAAREQRSQAEQLRRREHLLAQWEL
EVFERELTLLLQQVDRERPHVRRRRGTFKRSKLRARDGGERISMPLDFKHRITVQASP
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Primates;
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Pred. No. 5.6e-14;
0; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N. Louis, M.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Genome
                                                                                                                                                                                                                                                                             Lu, X., Garcia,
, J., Yu, W.,
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Search completed: December 13, Job time : 3037 secs
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                    2 CACCGGGACATCAAGGCAGGAAATATTTTGCTACTTGAGAAGATAGAACATGATGACATC 61
                                                                                                                                                                                                                                                                         TGCAATAAAACTTTGAAGATTACAGATTTTGGGTTGGCGAGGGAATGGCACAGGACCACC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="meplks:telksplgswngsgsggggggggggpegspkaagyanp"
/translation="meplks:telksplgswngsgsggggggggggpegspkaagyanp"
/translation="meplks:telksplaalsgbewaagoygggvglpeskyvsk"
gggpppecevasfgelleevigiggggvyrgswngsgelleevigspheskyvsk
gggpppecevasfgelleevigiggggvyrgspklubeltagrkypphylvww
AvQlargmhtihcealvpvihkdlksunilllopiesbumehktikitdeglarwemk
AvQlargmhtihcealvpvihkdlksunilllopiesbumehktikitdeglarwemk
AvQLargmhtihcealvpvihkdlksunilllopiesbumehktikitdeglarwemk
TTQMSAAGTYAWMAPEVIKASTESKGSDWSFGVLLMELLTGEVVYRGIDCLAVAXGV
AVNKLTIPIPSTCPEPFAQLMADCWAQDDHRRDDFS.QLEQLEALEAQVLREMPROSF
HSWQBEWKREIQGLDDELRAKEKELLSREEELTRAAREGRSQAEQLEALEAQVLREMPROSF
HSWQBEWKREIQGLDDELRAKEKELLSREEELTRAAREGRSQAEQLEALEAQVLREMPROSF
GLDRRRNVFEWGBQSFTFPRFTAIQLEDAEPGQAWGROSFRLEDSSNOERRACWAW
GPSSPKFGEAQNGRRRSGMDEXTWYLDSDDSSPLGSSSTPALHQNPRRSLEPEEPK
RPVPAERGSSGTPKLIQRALLRGTALLASIGLGRDLQPPGGPGRERGESPTTPTTF
PAACCPEEPPSSPLICFSLKTDSPFTAAPLLLDLGIPWGFVSAKSPRREEEPRGGTVS
PPPGTSRSAGGTPGTERSPPLGLISRRRPSPLASIGIDWSFVSAGPRPSPLPSPQPAP
PPGTSRSAGGTPGTERSPPLGLISRRRPSPLASIGIDWSFVSAGPRFSPLPSSQPAP
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/tissue_type="Brain, anaplastic c
1p/19q loss"
/clone_lib="NCI_CGAP_Brn67"
/lab_host="DH10B"
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/db_xref="GI:15030037"
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kinase kinase 11"
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494. .3037
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Pred. No. 5.
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